

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

(i) APPLICANT: Gruys, Kenneth J.

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Padgett, Stephen R.

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Fry, Joyce E.

Howe, Arlene R.

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(ii) TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
in Bacteria and Plants

(iii) NUMBER OF SEQUENCES: 11

25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB

(B) STREET: 800 North Lindbergh Boulevard

(C) CITY: St. Louis

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(D) STATE: Missouri

(E) COUNTRY: USA

(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 13-MAR-1996

## (viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 29,283

(C) REFERENCE/DOCKET NUMBER: 38-21(13585)A

## (ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GCGGCGCAG GTTACGCCG TACAAAAAAT GAAAAAAGTG 120

	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGGAAG ATCGCCAGCC AGTGCAACAGC	180
	TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC	240
5	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTTCT TTCTGCGCGG	300
	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
10	CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC	540
15	GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
	AAACAAGTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG	660
20	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
	GGCGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT	840
25	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960
30	TTCCACGGCC TGCCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCGTTCCG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT	1140
35	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260

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5 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320

CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

5 TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGG GCGTACTGGC GGCGTTCGAA 1440

CTTGCGGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

10 GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

## (2) INFORMATION FOR SEQ ID NO:2:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## 20 (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGGATC CGATATCTTA ACCCGCCAAA AAGAACCTGA ACGCCG

46

## 30 (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTGGATC CATGGCTGAC TCGCAACCCC TGTCGGG

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10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20 (A) DESCRIPTION: /desc = "synthetic DNA"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCTTCGAG TTCCCGGAAT CACCGGGCGC GTTCCTGCGC TTCC

44

(2) INFORMATION FOR SEQ ID NO:5:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60  
 CTGCGCGCGC CGGTTTACGA GCGGCGCAG GTTACGCCGC TACAAAAAAT GAAAAAACTG 120  
 TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGGAAG ATCGCCAGCC AGTGCACAGC 180  
 10 TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240  
 GCGGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300  
 15 TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360  
 CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420  
 AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480  
 20 ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540  
 GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600  
 25 AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660  
 AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720  
 GCGGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780  
 30 GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840  
 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900  
 35 GCCCTGCACA ACATTGCGCG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC 960  
 TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

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TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

GGGCGTTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140

5 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTGAGTTTC 1320

10 CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGC GTTCGAA 1440

15 CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

(2) INFORMATION FOR SEQ ID NO:6:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 TATCGCAGCC ACGGCACCGA CTACGGGCGC GTACTGGCGG CGTTCGAATT TGGCGACCAT 60

GAACC 65

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1545 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAACTG 120

20

TCGTGCGGTC TTGATAACGT CATTCTGGTG AAGCGGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG 300

25

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

30

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTGCGTGGC GGTGCTGATC 600

35

AAACAAGTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720



GGCGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780

GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840

5 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900

GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC 960

10 TTCCACGGCC TGCGCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140

15 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

20 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320

CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

TCTTTGTTC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GCGGTTTCGAA 1440

25 TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGGGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAACTG 120

TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG 300

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780

GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840

GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900

GCCCTGCACA ACATTGCGCG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC 960

TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

5 GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140

GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

10 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC 1320

CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

15 TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGC GTTCGAA 1440

TTTGCGGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACGCGTG AAGTGGTAGT GGTAAGCGGT GTCCGTACCG CGATCGGGAC CTTTGGCGGC 60

	AGCCTGAAGG ATGTGGCACC GCGGAGCTG GCGCACTGG TGGTGCGCGA GGCCTGGCG	120
	CGCGCGCAGG TGTCGGGCGA CGATGTCGGC CACGTGGTAT TCGGCAACGT GATCCAGACC	180
5	GAGCCGCGCG ACATGTATCT GGGCCGCGTC GCGGCCGTCA ACGGCGGGT GACGATCAAC	240
	GCCCCGCGC TGACCGTGAA CCGCCTGTGC GGCTCGGGCC TGCAGGCCAT TGTCAGCGCC	300
	GCGCAGACCA TCCTGCTGGG CGATACCGAC GTCGCCATCG GCGGCGGCGC GGAAAGCATG	360
10	AGCCGCGCAC CGTACCTGGC GCCGGCAGCG CGCTGGGGCG CACGCATGGG CGACCCGGC	420
	CTGGTCGACA TGATGCTGGG TGCCTGTCAC GATCCCTTCC ATCGCATCCA CATGGGCGTG	480
15	ACCGCCGAGA ATGTCGCCAA GGAATACGAC ATCTCGCGCG CGCAGCAGGA CGAGCCGCG	540
	CTGGAATCGC ACCGCCGCGC TTCGGCAGCG ATCAAGGCCG GCTACTTCAA GGACCAGATC	600
	GTCCCGGTGG TGAGCAAGGG CCGCAAGGGC GACGTGACCT TCGACACCGA CGAGCACGTG	660
20	CGCCATGACG CCACCATCGA CGACATGACC AAGCTCAGGC CGGTCTTCGT CAAGGAAAAC	720
	GGCACGGTCA CGGCCGGCAA TGCCTCGGGC CTGAACGACG CCGCCGCCGC GGTGGTGATG	780
25	ATGGAGCGCG CCGAAGCCGA GCGCCGCGGC CTGAAGCCGC TGGCCCGCCT GGTGTCGTAC	840
	GGCCATGCCG GCGTGGACCC GAAGGCCATG GGCATCGGCC CCGTGCCGGC GACGAAGATC	900
	GCGCTGGAGC GCGCCGGCCT GCAGGTGTCG GACCTGGACG TGATCGAAGC CAACGAAGCC	960
30	TTTGCCGCAC AGGCGTGC GC GTGACCAAG GCGCTCGGTC TGGACCCGGC CAAGGTTAAC	1020
	CCGAACGGCT CGGGCATCTC GCTGGGCCAC CCGATCGGCG CCACCGGTGC CCTGATCAG	1080
35	GTGAAGGCGC TGCATGAGCT GAACCGCGTG CAGGGCCGCT ACGCGCTGGT GACGATGTGC	1140
	ATCGGCGGCG GGCAGGGCAT TGCCGCCATC TTCGAGCGTA TCTGA	1185

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## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Arg Glu Val Val Val Ser Gly Val Arg Thr Ala Ile Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Arg Glu Val Val Val Ser Gly Val Arg Thr Ala Ile Gly  
1 5 10 15

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala  
20 25 30

Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp  
 35 40 45

5 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp  
 50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn  
 65 70 75 80

10 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala  
 85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala  
 15 100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro  
 115 120 125

20 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met  
 130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val  
 145 150 155 160

25 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln  
 165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys  
 30 180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg  
 195 200 205

35 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala  
 210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn

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225                      230                      235                      240  
 Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala  
                                  245                      250                      255  
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 Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys  
                                  260                      265                      270  
 Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys  
 10                      275                      280                      285  
 Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg  
                                  290                      295                      300  
 15  
 Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala  
 305                      310                      315                      320  
 Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro  
                                  325                      330                      335  
 20  
 Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile  
                                  340                      345                      350  
 Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn  
 25                      355                      360                      365  
 Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly  
                                  370                      375                      380  
 30  
 Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile  
 385                      390

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